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39. (amended) A kit for amplifying *Mycobacterial* nucleic acid, containing at least one of a first and second oligonucleotide; said first oligonucleotide comprising xGCCGTCACCCCACCAACAAGCT (SEQ ID: 1 or 22), and said second oligonucleotide comprising xGGGATAAGCCTGGGAAACTGGGTCTAATACC (SEQ ID: 2), wherein x is nothing or is a sequence recognized by an RNA polymerase and each said oligonucleotide is about 22 to about 100 bases in length.

- 40. (amended) An oligonucleotide of about 20 to about 100 bases in length comprising a nucleic acid sequence selected from the group consisting of xGCCGTCACCCACCAACAAGCT (SEQ ID: 1 or 22), xGGGATAAGCCTGGGAAACTGGGTCTAATACC (SEQ ID: 2), [xCCAGGCCACTTCCGCTAACC (SEQ ID: 6), xCGCGGAACAGGCTAAACCGCACGC (SEQ ID: 7),] and their fully complementary sequences of the same length, wherein x is nothing or is a sequence recognized by an RNA polymerase.
- 41. (amended) A kit for amplifying and detecting *Mycobacterial* nucleic acid, containing a first oligonucleotide of about 24 to about 100 bases in length comprising a nucleotide base sequence GTCTTGTGGTGGAAAGCGCTTTAG (SEQ ID: 3) and one or more of second oligonucleotides of about 23 to about 100 bases in length/selected from the group consisting of xGCCGGTCACCCACCAACAAGCT (SEQ ID: 1 or 22) and xGGATAAGCCTGGGAAACTGGGTCTAATACC (SEQ ID: 2), wherein x is nothing or is a sequence recognized by an RNA polymeruse.
- 42. (amended) A kit for amplifying and detecting *Mycobacterial* nucleic acid, containing a first oligonucleotide of about 23 to about 100 bases in length comprising a nucleotide base sequence GGAGGATATGTCTCAGCGCTACC (SEQ ID: 8) and one or more of second oligonucleotides of about 20 to about 100 bases in length selected from the group consisting of xCCAGGCCACTTCCGCTAACC (SEQ ID: 6 on 23) and xCGCGGAACAGGCTAAACCGCACGC (SEQ ID: 7), wherein x is nothing or is a sequence recognized by an RNA polymerase.

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- 67. (amended) A[n] <u>primer</u> oligonucleotide from 10 to 100 nucleotide[s] <u>bases</u> in length able to [bind to or extend through] <u>hybridize to</u> a region of *Mycobacterium tuberculosis* nucleic acid, wherein said region consists of a nucleotide base sequence selected from the group consisting of SEQ ID NO: 2, [SEQ ID NO: 7,] SEQ ID NO: 22 [and SEQ ID NO: 23], and their fully complementary sequences of the same length.
- 68. (amended) The <u>primer</u> oligonucleotide of claim 67, wherein the <u>primer oligonucleotide</u> is from 15 to 50 nucleotides in length.
- 69. (amended) The <u>primer</u> oligonucleotide of claim 67, comprising a nucleotide base sequence selected from the group consisting of SEQ ID NO: 2, [SEQ ID NO: 7,] SEQ ID NO: 22 [and SEQ ID NO: 23], and their fully complementary sequences of the same length.
- 70. (amended) The <u>primer</u> oligonucleotide of claim 67, consisting of <u>or contained within</u> a nucleotide base sequence selected from the group consisting of SEQ ID NO: 2, [SEQ ID NO: 7,] SEQ ID NO: 22 [and SEQ ID NO: 23], and their fully complementary sequences of the same length.
- 71. (amended) The <u>primer</u> oligonucleotide of claim 67 which <u>further</u> comprises, in the 5' upstream region, a[n oligo] nucleotide sequence which is recognizable by an RNA polymerase and enhances initiation or elongation by said RNA polymerase.
- 72. (amended) The <u>primer</u> oligonucleotide of claim 71, comprising a nucleotide base sequence selected from the group consisting of SEQ ID NO: 1[, SEQ ID NO: 6] and SEQ ID NO: 19.
- 73. (amended) The <u>primer</u> oligonucleotide of claim 71, consisting of <u>or contained within</u> a sequence selected from the group consisting of SEQ ID NO: 1[, SEQ ID NO: 6] and SEQ ID NO: 19.
- 74. (amended) A composition able [to amplify] for amplification of Mycobacterium tuberculosis nucleic acid, comprising: one or more <u>primer</u> oligonucleotides from about 10 to about 100 nucleotide bases in length which will, under nucleic acid amplification conditions, [bind to or

extend through] <u>hybridize to</u> a region of *Mycobacterium tuberculosis* nucleic acid consisting of a nucleotide base sequence, said region selected from the group consisting of:

- a) SEQ ID NO: 23,
- b) [SEQ ID NO: 8,
- c)] SEQ ID NO: 7, and
- [d) SEQ ID NO: 9,
- e) SEQ ID NO: 10, and
- f] c) [the] a nucleotide sequence[s] perfectly complementary to [these] a sequence[s] of part (a) or (b).
- 75. (amended) The composition of claim 74 comprising two or more of said primer oligonucleotides
- 76. (amended) The composition of claim 74 comprising a first <u>primer</u> oligonucleotide which comprises a nucleotide base sequence selected from the group consisting of SEQ ID NO: 23[,] and SEQ ID NO: 7.
- 77. (amended) The composition of claim 76 <u>further</u> comprising a second <u>primer</u> oligonucleotide which comprises a nucleofide base sequence <u>different from that of the first primer</u> <u>oligonucleotide</u>, wherein the nucleotide base sequence of the second primer oligonucleotide is selected from the group consisting of SEQ ID NO: 23[,] and SEQ ID NO: 7.
- 78. (amended) The composition of any one of claims 74, 75, or 76, wherein one or more <u>primer</u> oligonucleotides further comprises, in the 5' upstream region, a nucleotide base sequence which is recognized by an RNA polymerase and which enhances transcription initiation or polymerization by said RNA polymerase.
- 79. (amended) The composition of any one of claims 74, 76, or 77, further comprising a nucleic acid hybridization assay probe from about 10 to about 100 nucleotide bases in length which will hybridize with at least 10 contiguous bases of a nucleotide base sequence region of *Mycobacterium tuberculosis* nucleic acid to form a detectable duplex under hybridization

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conditions[;], wherein said region is selected from the group consisting of SEQ ID NO: 8 and the perfectly complementary sequence thereto.

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- 82. (amended) The composition of claim 79 or 80 wherein said probe contains a detectable •
- 84. (amended) A composition able [to amplify] for amplification of Mycobacterium tuberculosis nucleic acid, comprising: one or more primer oligonucleotides from about 10 to about 100 nucleotide bases in length which will, under nucleic acid amplification conditions, [bind to or extend through] hybridize to a region of Mycobacterium tuberculosis nucleic acid consisting of a nucleotide base sequence, said region selected from the group consisting of:
 - a) SEQ ID NO: 22,
 - b) [SEQ ID NO: 3,
 - c)] SEQ ID NO: 2, and
 - [d) SEQ ID NO: 4,
 - e) SEQ ID NO 5, and
- f] \underline{c}) [the] \underline{a} nucleotide sequence[s] perfectly complementary to [these] \underline{a} sequence[s] \underline{of} part (a) or (b).
- 85. (amended) The composition of claim 84 comprising two or more of said primer oligonucleotides.
- 86. (amended) The composition of claim 84 comprising a first <u>primer</u> oligonucleotide which comprises a nucleotide base sequence selected from the group consisting of SEQ ID NO: 22[,] and SEQ ID NO: 2.
 - 87. (amended) The composition of claim 86 <u>further</u> comprising a second <u>primer</u> oligonucleotide which comprises a nucleotide base sequence <u>different from that of the first primer</u> oligonucleotide, wherein the nucleotide base sequence of the second primer oligonucleotide is selected from the group consisting of SEQID NO: 22[,] and SEQ ID NO: 2.

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88. (amended) The composition of any one of claims 84, 85, or 86, wherein one or more primer oligonucleotides further comprises, in the 5' upstream region, a nucleotide base sequence which is recognized by an RNA polymerase and which enhances transcription initiation or polymerization by said RNA polymerase.

- 89. (amended) The composition of any one of claims 84, 86, or 87, further comprising a nucleic acid hybridization assay probe from about 10 to about 100 nucleotide bases in length which will hybridize with at least 10 contiguous bases of a nucleotide base sequence region of *Mycobacterium tuberculosis* nucleic acid to form a detectable duplex under hybridization conditions[;], said region consisting of SEQ ID NO: 3 or the perfectly complementary sequence thereto.
- 91. (amended) The composition of claim 89 or 90, wherein said probe comprises an oligonucleotide selected from the group consisting of SEQ ID NO: 3 and the perfectly complementary sequence thereto.

100. (amended) A kit for amplifying *Mycobacterial* nucleic acid, containing a first of gonucleotide comprising xCCAGGCCACTTCCGCTAACC (SEQ ID: 6 or 23), and a second oligonucleotide comprising x[']CGCGGAACAGGCTAAACCGCACGC (SEQ ID: 7), wherein x is nothing or is a sequence recognized by an RNA polymerase [and x' is nothing or is a sequence recognized by an RNA polymerase].

- 101. (amended) A composition useful in the detection of *Mycobacterium tuberculosis* comprising at least one oligonucleotide, or composition containing an oligonucleotide, selected from the group consisting of:
- a) a nucleic acid hybridization assay probe from about 10 to about 100 nucleotide bases in length comprising an oligonucleotide which will hybridize to at least 10 contiguous bases of a nucleotide base sequence region of a target *Mycobacterium tuberculosis* nucleic acid, said region selected from the group consisting SEQVD NO: 3, SEQ ID NO: 8, and the <u>nucleotide</u> sequences perfectly complementary thereto; <u>and</u>

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- b) [an] at least one primer oligonucleotide from about 10 to about 100 nucleotide bases in length able to [bind to ar extend through] hybridize to a region of *Mycobacterium tuberculosis* nucleic acid, said region consisting of a nucleotide base sequence selected from the group consisting of [SEQ ID NO: 1,] SEQ ID NO: 2, [SEQ ID NO: 3, SEQ ID NO: 4, SEQ ID NO: 5, SEQ ID NO: 6,] SEQ ID NO: 7, [SEQ ID NO: 8, SEQ ID NO: 9, SEQ ID NO: 10,] SEQ ID NO: 22, SEQ ID NO: 23, and the <u>nucleotide</u> sequences perfectly complementary to these sequences[,
 - c) a kit comprising the oligonucleotide of b), and
- d) a specifically detectable nucleic acid hybrid formed under nucleic acid hybridization conditions between the hybridization assay probe of a) and a nucleic acid comprising a *Mycobacterium tuberculosis* nucleotide case sequence].

B. Please add the following new claims:

143. (new) An oligonucleotide of about 20 to about 100 bases in length comprising a nucleic acid sequence selected from the group consisting of xCCAGGCCACTTCCGCTAACC (SEQ ID: 6 or 28), xCGCGGAACAGGCTAAACCGCACGC (SEQ ID: 7), and their fully complementary sequences of the same length, wherein x is nothing or is a sequence recognized by an RNA polymerase.

- 144. (new) The plurality of oligonucleotides of claim 143, wherein one or more of said oligonucleotides is modified at 3' end to reduce or block extension of said one or more of said oligonucleotides by a polymerase.
- 145. (new) A plurality of oligonucleotides of claim 143, wherein one or more of said oligonucleotides is unmodified at 3' end and one or more of said oligonucleotides is modified at 3' end to reduce or block extension by a palymerase.
- 146. (new) The plurality of oligonucleotides of claim 145, wherein one or more of said oligonucleotides is differently modified at 3' end to reduce or block extension by a polymerase.

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- 147. (new) A primer oligonucleotide from 10 to 100 nucleotide bases in length able to hybridize to a region of *Mycobacterium tuberculosis* nucleic acid, wherein said region consists of a nucleotide base sequence selected from the group consisting of SEQ ID NO: 7, SEQ ID NO: 23, and their fully complementary sequences of the same length.
- 148. (new) The primer oligonucleotide of claim 147, wherein the primer oligonucleotide is from 15 to 50 nucleotides in length.
- 149. (new) The primer oligonucleotide of claim 147, wherein the primer oligonucleotide is from about 20 to about 100 nucleotides in length.
- 150. (new) The primer oligonucleotide of claim 69, wherein the primer oligonucleotide is from about 20 to about 100 nucleotides in length.
- 151. (new) The primer oligonucleotide of claim 147, comprising a nucleotide base sequence selected from the group consisting of SEQ ID NO: 7, SEQ ID NO: 23, and their fully complementary sequences of the same length.
- 152. (new) The primer of igonucleotide of claim 147, consisting of or contained within a nucleotide base sequence selected from the group consisting of SEQ ID NO: 7, SEQ ID NO: 23, and their fully complementary sequences of the same length.
- 153. (new) The primer oligonucleotide of claim 147 which further comprises, in the 5' upstream region, a nucleotide sequence which is recognizable by an RNA polymerase and enhances initiation or elongation by said RNA polymerase.
- 154. (new) The primer oligonucleotide of claim 153, comprising a nucleotide base sequence selected from the group consisting of SEQ ID NO: Land SEQ ID NO: 19.
- 155. (new) The primer oligonucleotide of claim 153, consisting of or contained within a sequence selected from the group consisting of SEQ ID NO: 6 and SEQ ID NO: 19.



- 156. (new) The composition of claim 82 further comprising first and second helper oligonucleotides wherein the first helper oligonucleotide comprises SEQ ID NO: 9 and the second helper oligonucleotide comprises SEQ ID NO: 10.
- 157. (new) The composition according to claim 101 further comprising at least one helper probe comprising a nucleotide sequence selected from the group consisting of SEQ ID NO:4, SEQ ID NO:5, SEQ ID NO:9, SEQ ID NO: 10, and the nucleotide sequences perfectly complementary to these sequences.
 - 158. (new) A kit comprising a primer oligonucleotide of claim 101.
- 159. (new) A composition comprising a specifically detectable nucleic acid hybrid formed under nucleic acid hybridization conditions between the nucleic acid hybridization assay probe of claim 101 and a nucleic acid comprising a *Mycobacterium tuberculosis* nucleotide base sequence.
- 160. (new) A composition useful in the detection of *Mycobacterium tuberculosis* comprising at least one oligonucleotide, or composition containing an oligonucleotide, selected from the group consisting of:
- a) a nucleic acid hybridization assay probe from about 10 to about 100 nucleotide bases in length comprising an oligonucleotide which will hybridize to at least 10 contiguous bases of a nucleotide base sequence region of a target *Mycobacterium tuberculosis* nucleic acid, said region selected from the group consisting SEQ ID NO: 3 and the nucleotide sequences perfectly complementary thereto; and
- b) at least one primer oligonucleotide from about 10 to about 100 nucleotide bases in length able to hybridize to a region of *Mycobacterium tuberculosis* nucleic acid, said region consisting of a nucleotide base sequence selected from the group consisting of SEQ ID NO: 1, SEQ ID NO: 22, SEQ ID NO: 2, and the nucleotide sequences perfectly complementary to these sequences.
- 161. (new) The composition according to claim 160 further comprising at least one helper probe comprising a nucleotide sequence selected from the group consisting of SEQ ID NO:4, SEQ ID NO:5, and the nucleotide sequences perfectly complementary to these sequences.

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- 162. (new) A kit comprising a primer oligonucleotide of claim 160.
- 163. (new) A composition comprising a specifically detectable nucleic acid hybrid formed under nucleic acid hybridization conditions between the nucleic acid hybridization assay probe of claim 160 and a nucleic acid comprising a *Mycobacterium tuberculosis* nucleotide base sequence.
- 164. (new) A composition useful in the detection of *Mycobacterium tuberculosis* comprising at least one oligonucleotide, or composition containing an oligonucleotide, selected from the group consisting of:
- a) a nucleic acid hybridization assay probe from about 10 to about 100 nucleotide bases in length comprising an oligonacleotide which will hybridize to at least 10 contiguous bases of a nucleotide base sequence region of a target *Mycobacterium tuberculosis* nucleic acid, said region selected from the group consisting SEQ ID NO: 8 and the nucleotide sequences perfectly complementary thereto; and
- b) at least one primer oligonucleotide from about 10 to about 100 nucleotide bases in length able to hybridize to a region of *Mycobacterium tuberculosis* nucleic acid, said region consisting of a nucleotide base sequence selected from the group consisting of SEQ ID NO: 6, SEQ ID NO: 23, SEQ ID NO: 7, and the nucleotide sequences perfectly complementary to these sequences.
- 165. (new) The composition according to claim 164 further comprising at least one helper probe comprising a nucleotide sequence selected from the group consisting of SEQ ID NO:9, SEQ ID NO:10, and the nucleotide sequences perfectly complementary to these sequences.
 - 166. (new) A kit comprising a primer oligonucleotide of claim 164.
- 167. (new) A composition comprising a specifically detectable nucleic acid hybrid formed under nucleic acid hybridization conditions between the nucleic acid hybridization assay probe of claim 164 and a nucleic acid comprising a *Mycobacterium tuberculosis* nucleotide base sequence.

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